

1 GACGCGGCTGGCACTGGGTGGGCGCCACACGCTCGGCCACAAC TCCCGGGGCTTCGGCG 60  
 1 R G W H W V G A H T L G H N S R G F G V 20  
 61 TGGCCATAGTGGGCAACTACACCGCGGCGCTGCCCACCGAGGCCGCTCTGCGCACGGTGC 120  
 21 A I V G N Y T A A L P T E A A L R T V R 40  
 121 GCGACACGCTCCCGAGTTGTGCGGTGCGCGCGGCCTCCTGCGGCCAGACTACGCGCTGC 180  
 41 D T L P S C A V R A G L L R P D Y A L L 60  
 181 TGGGCCACCGCCAGCTGGTGGCACCAGACTGCCCCGGCGACGCGCTCTTCGACCTGCTGC 240  
 61 G H R Q L V R T D C P G D A L F D L L R 80  
 241 GCACCTGGCCGCACTTCACCGCGGTGAGTCTTCGCAGCCTGCACTACACGGCCCGCCGCC 300  
 81 T W P H F T A V S L R S L H Y T A R R P 100  
 301 CCTCCGTCTACACAAGCTCCACGAGGCCCTGCCCCCTGCCTGTAACAGCTGTGCCCGCA 360  
 101 S V Y T S S T R P L P P A C N S C A R T 120  
 361 CAGCCTCAGCCAGGCCCCCAACTTCCCGGCGGCACGTCTATT CAGGAAACCTAGGCCAG 420  
 121 A S A R P P T S R R H V Y S G N L G P A 140  
 421 CCTTTGCGGGTCACTCTGCGGGCAACATCCCTGATCCTGTGACTTCTGCCTATGCAGCCT 480  
 141 F A G H S A G N I P D P V T S A Y A A S 160  
 481 CAGCTCAGCCCCAGACCCAGCCAGCCTGTCCTTTCCCCAGCTCCTAATACCTCTACCTTT 540  
 161 A Q P Q T Q P A C P F P S S 174  
 541 CCAGCCAAGGCATGGACCCTGACACCTGCCAACAGCCCCTCTGCCCTCACAACCTCAGCC 600  
 601 TGGCCTTCATGACTTCTCTACCCAAGTCACAACCTGTCAGGCTGCACCACCTCATCCTGG 660  
 661 CCCGCCGAACCTTGACCTCACCCCTGCCCTACCCGAAGGCTCTCTGTCCACACAACATG 720

FIG. 1A

721 AACCTAGGCTGTGACCTTTTGCCTTCACAACCTCTGTCCAGTCCTTAATCCTGTGTTGCA 780  
781 ATTCTCTGTCCAGACAATCTCAACTCTGAGGTTGCTTGTTCGTCCCTGACTCCTTAACC 840  
841 CCTGATGACAACCTCTTATGCCAGCACAACTTTGACCTGATGACCTCATCCCAGCCCTTGA 900  
901 TCGCCATCACTAAAACAATTTTAGAATCACACCTGGACAATCTCGTGCTACCTACATACT 960  
961 GCCACTCCATTTTCAATTAAGCTATTGACTAGCACATCCATCTCGGCCTATAGTTGGCTTTG 1020  
1021 TCCTCACTCTCTCACTTTGGGCCACTGTCCCCTCCCTGATAAAGGGGATATCACCACCGA 1080  
1081 TCCCACAGAAATACAACTACCATCAGAGAATACTATAAACACCTCTATGCAAATAAACT 1140  
1041 AGAAAATCTAGAAGAAATGGATAAATTCCTCAACACCCACTACCAAAAAAAAAAAAAAAAAA 1200

**FIG. 1B**

1 GCCGTTATGTGAGGTAAGCAGCTTTCTCCAACAGAAGTTCCTCTCTCCTCAAAGGCCAG 60  
 61 AGTGTCCAGGCCAACCAACTGACCAAGAATTACAACTGCTGAACTGGCCTCCGAGGTT 120  
 121 TCTGCTGGGTCTGTGCCCTGGAAGTGGAGACCCACCATGAAGGCCTGGGGTGGCCTCTGG 180  
 1 M K A W G A L W 8  
 181 ATCGTGCTTGATTGCTGCTGTGGCCAGAGCCAGGGGCAGCCTCCTCCTTGCCCTCTGCTC 240  
 9 I V L G L L L W P E P G A A S S L P L L 28  
 241 ATGGAATCATCATCCAGGCCCTTGCTGAACTTGAGCAAAAGGTACCAGTGAAGGCC 300  
 29 M D S I I Q A L A E L E Q K V P V T E A 48  
 301 AGCATCACTGCCTCTGCATGGATTCTGTGAGCCAAGAACTCCAGCACCCACAATTCCTT 360  
 49 S I T A S A W I L S A K N S S T H N S L 68  
 361 CACCAGCGCTTGCTGCTGAAGGCACCAAGCCACAACACTACAGAGCCAGATCCTCACTCT 420  
 69 H Q R L L L K A P S H N T T E P D P H S 88  
 421 CTCAGCCCGGAGCTTCAAGCACTGATTTCTGAGGTGGCTCAACACGATGTACAGAATGGG 480  
 89 L S P E L Q A L I S E V A Q H D V Q N G 108  
 481 CGGGAATATGGAGTGGTGTGGCACCTGATGGCTCCACCGTAGCTGTGAAGCCTCTGCTG 540  
 109 R E Y G V V L A P D G S T V A V K P L L 128  
 541 TTTGGGCTAGAGGCCGTCTACAGGCACACAGCGTTGCTAACTTGCCTTCAGATTGTCTG 600  
 129 F G L E A G L Q A H S V A N L P S D C L 148  
 601 GCTATCCCCTGTGATACTGGAGACACCTTGGCCAATATTAGAGCCACCTGGCCAGGACTC 660  
 149 A I P C D T G D T L A N I R A T W P G L 168  
 661 ATGGATGCTTTTCCAAATGCCTCTTCTCCAGATGTTGGAGCCACTTTACCAAACGACAAA 720  
 169 M D A F P N A S S P D V G A T L P N D K 188

FIG. 2A

721 GCCAAGACTCCCACCACTGTGGACAGACTCCTGGCAATCACCTTGGCTGGTGAAGTTAGGT 780  
 189 A K T P T T V D R L L A I T L A G D L G 208  
 781 CTGACCTTCCTCCACAGGTCCCAGACTTGGAGTCTCCAGGACTGGGAAGTGAAGGCTGC 840  
 209 L T F L H R S Q T W S P P G L G T E G C 228  
 841 TGGGACCAGCTTACTGCCCCAGGGTCTTCACACTGTGGACCCCCAGGCATCCAGGCTC 900  
 229 W D Q L T A P R V F T L L D P Q A S R L 248  
 901 ACCATGGCTTTTCCTCAATGGTGCCTTAGATGGAGCTCTCCTTGGGAACCACTTGAGCCAA 960  
 249 T M A F L N G A L D G A L L G N H L S Q 268  
 961 ATCCCTAGGCCCCACCCACCCCTCAGCCACCTGCTAAGAGAGTACTATGGAGCTGGGGTG 1020  
 269 I P R P H P P L S H L L R E Y Y G A G V 288  
 1021 AATGGAGATCCGGTGTTCGGAAGTAACTTCCGAAGGCAGAACGGTGCTGCTTTGACTTCA 1080  
 289 N G D P V F R S N F R R Q N G A A L T S 308  
 1081 GCCCCTACCCTGGCCCAGCAGGTATGGGAGGCCCTTGTCTGTACAGAACTGGAGCCA 1140  
 309 A P T L A Q Q V W E A L V L L Q K L E P 328  
 1141 GAACACCTACAGTTGCAGAACATTAGCCAAGAGCAGCTGGCTCAGGTAGCCACCTTGGCT 1200  
 329 E H L Q L Q N I S Q E Q L A Q V A T L A 348  
 1201 ACCAAGGAGTTCACTGAGGCTTTTCCTGGGATGCCAGCCATTACCCCCGCTGCCGTGG 1260  
 349 T K E F T E A F L G C P A I H P R C R W 368  
 1261 GGAGCGGCTCCCTACCGAGGCCACCCAACCACTCCGGCTGCCACTTGGATTCTTATAT 1320  
 369 G A A P Y R G H P T P L R L P L G F L Y 388  
 1321 GTGCATCACACATACGTGCCAGCGCCACCCTGCACCACCTTCCAGAGCTGCGCCGCCGAT 1380  
 389 V H H T Y V P A P P C T T F Q S C A A D 408

FIG. 2B

1381 ATGCGCTCCATGCAGCGTTTCCACCAGGATGTGCGCAAGTGGGATGACATCGGCTACAGT 1440  
 409 M R S M Q R F H Q D V R K W D D I G Y S 428  
 1441 TTCGTGGTAGGCTCCGACGGCTATCTGTACCAGGGCCGTGGCTGGCACTGGGTAGGTGCG 1500  
 429 F V V G S D G Y L Y Q G R G W H W V G A 448  
 1501 CACACACGCGGCTACAACTCCCGCGGCTTCGGTGTGGCCTTCGTGGGCAACTACACTGGG 1560  
 449 H T R G Y N S R G F G V A F V G N Y T G 468  
 1561 TCACTGCCCCAACGAAGCTGCGCTGAACACGGTGCGCGACGCGCTCCCGAGCTGCGCAATT 1620  
 469 S L P N E A A L N T V R D A L P S C A I 488  
 1621 CGCGAAGGTCTCTTGCGGCCAGACTACAAGCTGCTTGGCCACCGCCAGCTAGTGCTCACC 1680  
 489 R E G L L R P D Y K L L G H R Q L V L T 508  
 1681 CACTGCCCCGGAACGCGCTCTTCAACTTGCTGCGCACCTGGCCTCACTTCACAGAGGTT 1740  
 509 H C P G N A L F N L L R T W P H F T E V 528  
 1741 GAAACTAAGAACTCCTTTGAGAGACCCTTGAAGATCCAGGAGGTATTATCCCTGATGAT 1800  
 529 E N \* 531  
 1801 CCTTTGAGCAACCACAGACCTCCAATAAAGGGACCACTGAAAGGAAAAAAAAAAAAAAAA 1860  
 1861 AAAAAAAAAAAAAAAAAA 1876

FIG. 2C

		10	20	30	40	
1	-----					hPGRP-L aa Seq.
1	M K A W G A L W I V L G L L L W P E P G A A S S L P L L M D S I I Q A L A E L E					mPGRP-L aa Seq.
		50	60	70	80	
1	-----					hPGRP-L aa Seq.
41	Q K V P V T E A S I T A S A W I L S A K N S S T H N S L H Q R L L L K A P S H N					mPGRP-L aa Seq.
		90	100	110	120	
1	-----					hPGRP-L aa Seq.
81	T T E P D P H S L S P E L Q A L I S E V A Q H D V Q N G R E Y G V V L A P D G S					mPGRP-L aa Seq.
		130	140	150	160	
1	-----					hPGRP-L aa Seq.
121	T V A V K P L L F G L E A G L Q A H S V A N L P S D C L A I P C D T G D T L A N					mPGRP-L aa Seq.
		170	180	190	200	
1	-----					hPGRP-L aa Seq.
161	I R A T W P G L M D A F P N A S S P D V G A T L P N D K A K T P T T V D R L L A					mPGRP-L aa Seq.
		210	220	230	240	
1	-----					hPGRP-L aa Seq.
201	I T L A G D L G L T F L H R S Q T W S P P G L G T E G C W D Q L T A P R V F T L					mPGRP-L aa Seq.
		250	260	270	280	
1	-----					hPGRP-L aa Seq.
241	L D P Q A S R L T M A F L N G A L D G A L L G N H L S Q I P R P H P P L S H L L					mPGRP-L aa Seq.
		290	300	310	320	
1	-----					hPGRP-L aa Seq.
281	R E Y Y G A G V N G D P V F R S N F R R Q N G A A L T S A P T L A Q Q V W E A L					mPGRP-L aa Seq.

FIG. 3A



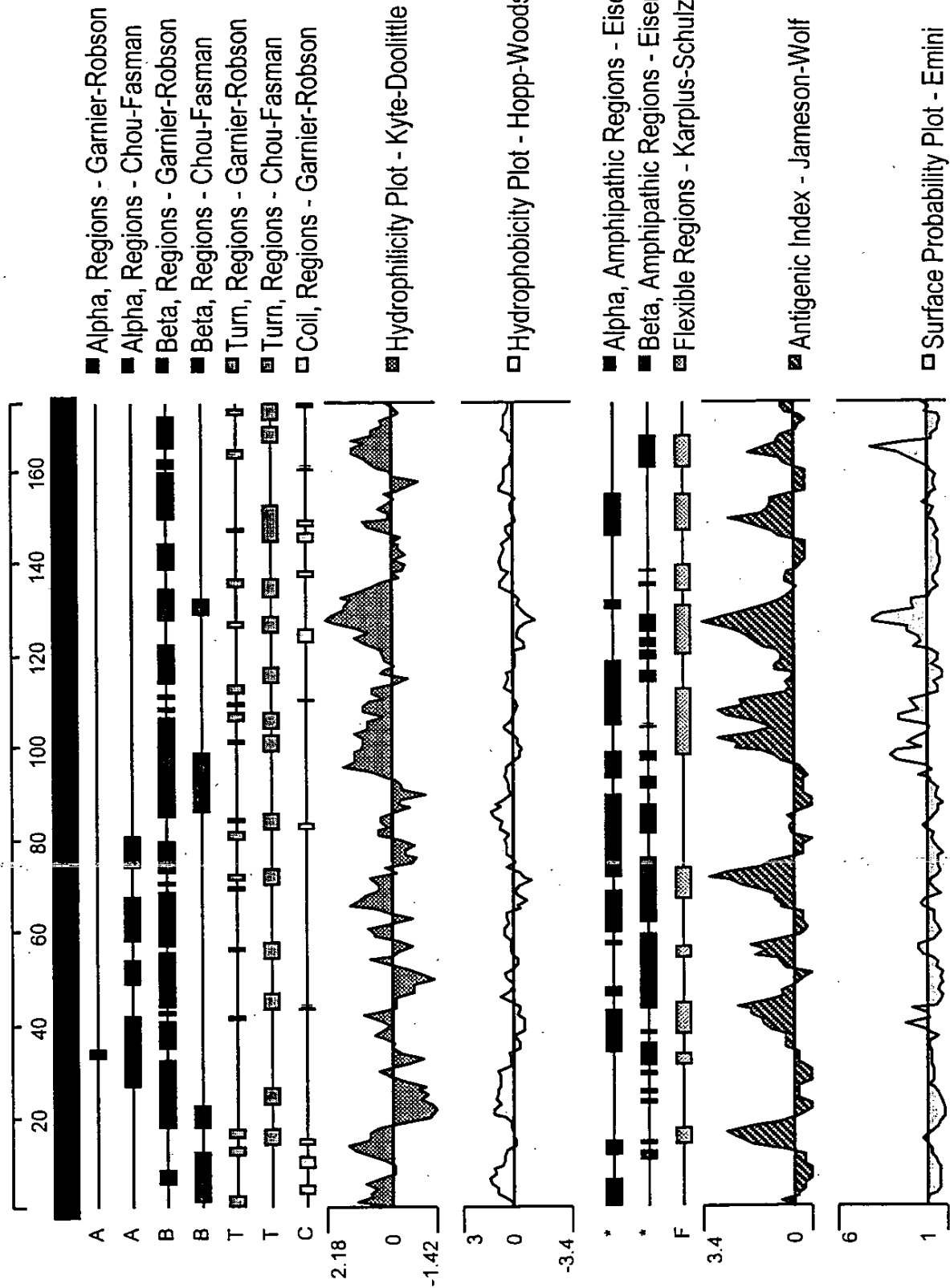


FIG. 4



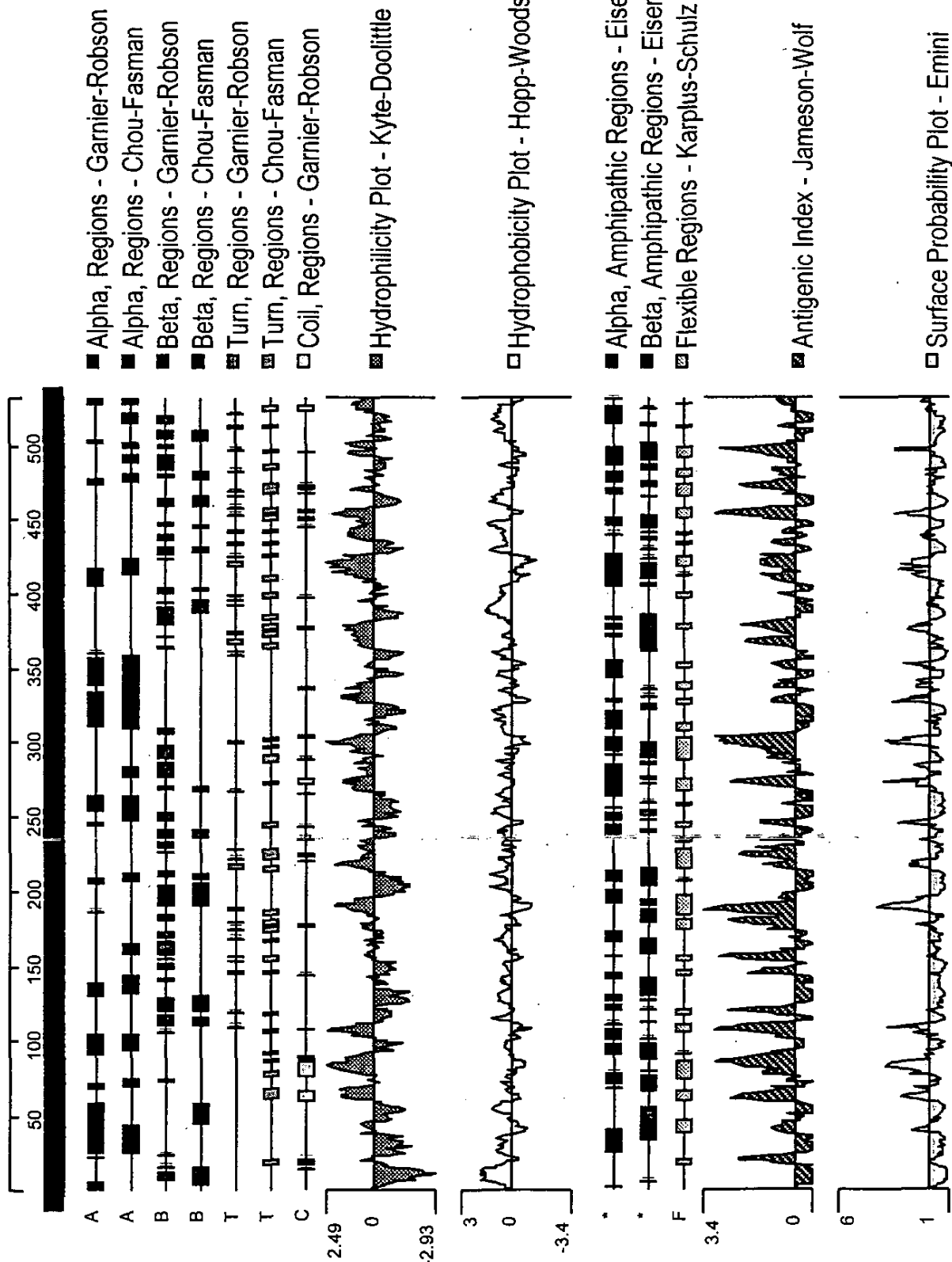


FIG. 5